0570
1204

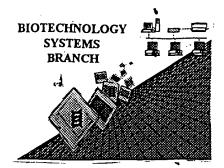# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/993,292_

Source: _01rt_

Date Processed by STIC: _12/3/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING   DATE: 12/03/2001
PATENT APPLICATION: US/09/993,292   TIME: 12:19:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\11212001\I993292.raw

Does Not Comply
Corrected Diskette Needed

Error on p. 5

```
      4 <110> APPLICANT: James E. Galen
      5        University of Maryland
      7 <120> TITLE OF INVENTION: USE OF CLY A HEMOLYSIN FOR EXCRETION OF
      8        PROTEINS
     10 <130> FILE REFERENCE: UOFMD.007A
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/993,292
C--> 12 <141> CURRENT FILING DATE: 2001-11-23
     12 <150> PRIOR APPLICATION NUMBER: 60/252,516
     13 <151> PRIOR FILING DATE: 2000-11-22
     15 <160> NUMBER OF SEQ ID NOS: 19
     17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 6271
     21 <212> TYPE: DNA
     22 <213> ORGANISM: Artificial Sequence
     24 <220> FEATURE:
     25 <223> OTHER INFORMATION: pSEC84 Expression Plasmid
     27 <400> SEQUENCE: 1
     28 gaattctgtg gtagcacaga ataatgaaaa gtgtgtaaag aagggtaaaa aaaaccgaat 60
     29 gcgaggcatc cggttgaaat aggggtaaac agacattcag aaatgaatga cggtaataaa 120
     30 taaagttaat gatgatagcg ggagttattc tagttgcgag tgaaggtttt gttttgacat 180
     31 tcagtgctgt caaatactta agaataagtt attgatttta accttgaatt attattgctt 240
     32 gatgttaggt gcttatttcg ccattccgca ataatcttaa aaagttccct tgcatttaca 300
     33 ttttgaaaca tctatagcga taaatgaaac atcttaaaag ttttagtatc atattcgtgt 360
     34 tggattattc tgcattttttg gggagaatgg acttgccgac tgattaatga gggttaatca 420
     35 gtatgcagtg gcataaaaaa gcaaataaag gcatataaca gatcgatctt aaacatccac 480
     36 aggaggatgg gatccaaaat aaggaggaaa aaaaaatgac tagtattttt gcagaacaaa 540
     37 ctgtagaggt agttaaaagc gcgatcgaaa ccgcagatgg ggcattagat ctttataaca 600
     38 aatacctcga ccaggtcatc ccctggaaga cctttgatga aaccataaaa gagttaagcc 660
     39 gttttaaaca ggagtactcg caggaagctt ctgttttagt tggtgatatt aaagttttgc 720
     40 ttatggacag ccaggacaag tattttgaag cgacacaaac tgtttatgaa tggtgtggtg 780
     41 tcgtgacgca attactctca gcgtatattt tactatttga tgaatataat gagaaaaaag 840
     42 catcagccca gaaagacatt ctcattagga tattagatga tggtgtcaag aaactgaatg 900
     43 aagcgcaaaa atctctcctg acaagttcac aaagtttcaa caacgcttcc ggaaaactgc 960
     44 tggcattaga tagccagtta actaatgatt tttcggaaaa aagtagttat ttccagtcac 1020
     45 aggtggatag aattcgtaag gaagcttatg ccggtgctgc agccggcata gtcgccggtc 1080
     46 cgtttggatt aattatttcc tattctattg ctgcgggcgt gattgaaggg aaattgattc 1140
     47 cagaattgaa taacaggcta aaaacagtgc aaaatttctt tactagctta tcagctacag 1200
     48 tgaaacaagc gaataaagat atcgatgcgg caaaattgaa attagccact gaaatagcag 1260
     49 caattgggga gataaaaacg gaaaccgaaa caaccagatt ctacgttgat tatgatgatt 1320
     50 taatgctttc tttattaaaa ggagctgcaa agaaaatgat taacacctgt aatgaatacc 1380
     51 aacaacgtca tggtaagaag acgcttttcg aggttcctga cgtcgctagc tgataacctа 1440
     52 gggccagcaa aaggccagga accgtaaaaa ggccgcgttg ctggcgtttt tccataggct 1500
     53 ccgcccccct gacgagcatc acaaaaatcg acgctcaagt cagaggtggc gaaacccgac 1560
     54 aggactataa agataccagg cgtttccccc tggaagctcc ctcgtgcgct ctcctgttcc 1620
     55 gaccctgccg cttaccggat acctgtccgc ctttctccct tcgggaagcg tggcgctttc 1680
     56 tcatagctca cgctgtaggt atctcagttc ggtgtaggtc gttcgctcca agctgggctg 1740
```

RAW SEQUENCE LISTING   DATE: 12/03/2001
PATENT APPLICATION: US/09/993,292   TIME: 12:19:47

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\11212001\I993292.raw**

```
 57 tgtgcacgaa cccccccgttc agcccgaccg ctgcgcctta tccggtaact atcgtcttga 1800
 58 gtccaacccg gtaagacacg acttatcgcc actggcagca gccactggta acaggattag 1860
 59 cagagcgagg tatgtaggcg gtgctacaga gttcttgaag tggtggccta actacggcta 1920
 60 cactagaagg acagtatttg gtatctgcgc tctgctgaag ccagttacct tcggaaaaag 1980
 61 agttggtagc tcttgatccg gcaaacaaac caccgctggt agcggtggtt tttttgtttg 2040
 62 caagcagcag attacgcgca gaaaaaaagg atctcaagaa gatcctttga tcttttctac 2100
 63 ggggtctgac gctcagtaga tctaaaacac taggcccaag agtttgtaga aacgcaaaaa 2160
 64 ggccatccgt caggatggcc ttctgcttaa tttgatgcct ggcagtttat ggcgggcgtc 2220
 65 ctgcccgcca ccctccgggc cgttgcttcg caacgttcaa atccgctccc ggcggatttg 2280
 66 tcctactcag gagagcgttc accgacaaac aacagataaa acgaaaggcc cagtctttcg 2340
 67 actgagcctt tcgtttttatt tgatgcctgg cagttcccta ctctcgcatg gggagacccc 2400
 68 acactaccat cggcgctacg gcgtttcact tctgagttcg gcatggggtc aggtgggacc 2460
 69 accgcgctac tgccgccagg caaattctgt tttatcagac cgcttctgcg ttctgattta 2520
 70 atctgtatca ggctgaaaat cttctctcat ccgccaaaac agccaagctg gatctggcaa 2580
 71 atcgctgaat attccttttg tctccgacca tcaggcacct gagtcgctgt ctttttcgtg 2640
 72 acattcagtt cgctgcgctc acggctctgg cagtgaatgg gggtaaatgg cactacaggc 2700
 73 gccttttatg gattcatgca aggaaactac ccataataca agaaaagccc gtcacgggct 2760
 74 tctcagggcg tttttatggcg ggtctgctat gtggtgctat ctgactttt gctgttcagc 2820
 75 agttcctgcc ctctgatttt ccagtctgac cacttcggat tatcccgtga caggtcattc 2880
 76 agactggcta atgcacccag taaggcagcg gtatcatcaa caggcttacc cgtcttactg 2940
 77 tcaaccggat ctaaaacact agcccaacct ttcatagaag gcggcggtgg aatcgaaatc 3000
 78 tcgtgatggc aggttgggcg tcgcttggtc ggtcatttcg aacccccagag tcccgctcag 3060
 79 aagaactcgt caagaaggcg atagaaggcg atgcgctgcg aatcgggagc ggcgataccg 3120
 80 taaagcacga ggaagcggtc agcccattcg ccgccaagct cttcagcaat atcacgggta 3180
 81 gccaacgcta tgtcctgata gcggtccgcc acacccagcc ggccacagtc gatgaatcca 3240
 82 gaaaagcggc cattttccac catgatattc ggcaagcagg catcgccatg ggtcacgacg 3300
 83 agatcctcgc cgtcgggcat gcgcgccttg agcctggcga acagttcggc tggcgcgagc 3360
 84 ccctgatgct cttcgtccag atcatcctga tcgacaagac cggcttccat ccgagtacgt 3420
 85 gctcgctcga tgcgatgttt cgcttggtgg tcgaatgggc aggtagccgg atcaagcgta 3480
 86 tgcagccgcc gcattgcatc agccatgatg gatactttct cggcaggagc aaggtgagat 3540
 87 gacaggagat cctgccccgg cacttcgccc aatagcagcc agtcccttcc cgcttcagtg 3600
 88 acaacgtcga gcacagctgc gcaaggaacg cccgtcgtgg ccagccacga tagccgcgct 3660
 89 gcctcgtcct gcagttcatt cagggcaccg gacaggtcgg tcttgacaaa aagaaccggg 3720
 90 cgcccctgcg ctgacagccg gaacacggcg gcatcagagc agccgattgt ctgttgtgcc 3780
 91 cagtcatagc cgaatagcct ctccacccaa gcggccggag aacctgcgtg caatccatct 3840
 92 tgttcaatca tgcgaaacga tcctcatcct gtctcttgat cagatcttga tcccctgcgc 3900
 93 catcagatcc ttggcggcaa gaaagccatc cagtttactt tgcagggctt cccaacctta 3960
 94 ccagagggcg ccccagctgg caattccggt tcgctgctag acaacatcag caaggagaaa 4020
 95 ggggctaccg gcgaaccagc agccccttta taaaggcgct tcagtagtca gaccagcatc 4080
 96 agtcctgaaa aggcgggcct gcgcccgcct ccaggttgct acttaccgga ttcgtaagcc 4140
 97 atgaaagccg ccacctccct gtgtccgtct ctgtaacgaa tctcgcacag cgattttcgt 4200
 98 gtcagataag tgaatatcaa cagtgtgaga cacacgatca acacacacca gacaagggaa 4260
 99 cttcgtggta gtttcatggc cttcttctcc ttgcgcaaag cgcggtaaga ggctatcctg 4320
100 atgtggacta gacataggga tgcctcgtgg tggttaatga aaattaactt actacggggc 4380
101 tatcttcttt ctgccacaca acacggcaac aaaccacctt cacgtcatga ggcagaaagc 4440
102 ctcaagcgcc gggcacatca tagcccatat acctgcacgc tgaccacact cactttccct 4500
103 gaaaataatc cgctcattca gaccgttcac gggaaatccg tgtgattgtt ccgcatcac 4560
104 gctgcctccc ggagtttgtc tcgagcactt ttgttacccg ccaaacaaaa cccaaaaaca 4620
105 acccataccc aacccaataa aacaccaaaa caagacaaat aatcattgat tgatggttga 4680
```

RAW SEQUENCE LISTING   DATE: 12/03/2001
PATENT APPLICATION: US/09/993,292   TIME: 12:19:47

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\11212001\I993292.raw**

```
106 aatggggtaa acttgacaaa caaacccact taaaacccaa aacatacccca aacacacacc 4740
107 aaaaaaacac cataaggagt tttataaatg ttggtattca ttgatgacgg ttcaacaaac 4800
108 atcaaactac agtggcagga aagcgacgga acaattaaac agcacattag cccgaacagc 4860
109 ttcaaacgcg agtgggcagt ctcttttggt gataaaaagg tctttaacta cacactgaac 4920
110 ggcgaacagt attcatttga tccaatcagc ccggatgctg tagtcacaac caatatcgca 4980
111 tggcaataca gcgacgttaa tgtcgttgca gtgcatcacg ccttactgac cagtggtctg 5040
112 ccggtaagcg aagtggatat tgtttgcaca cttcctctga cagagtatta cgacagaaat 5100
113 aaccaaccca atacggaaaa tattgagcgt aagaaagcaa acttccggaa aaaaattaca 5160
114 ttaaatggcg gggatacatt cacaataaaa gatgtaaaag tcatgcctga atctataccg 5220
115 gcaggttatg aagttctaca agaactggat gagttagatt ctttattaat tatagatctc 5280
116 gggggcacca cattagatat ttctcaggta atggggaaat tatcgggggat cagtaaaata 5340
117 tacggagact catctcttgg tgtctctctg gttacatctg cagtaaaaga tgcccttttct 5400
118 cttgcgagaa caaaaggaag tagctatctt gctgacgata taatcattca cagaaaagat 5460
119 aataactatc tgaagcaacg aattaatgat gagaacaaaa tatcaatagt caccgaagca 5520
120 atgaatgaag cacttcgtaa acttgagcaa cgtgtattaa atacgctcaa tgaattttct 5580
121 ggttatactc atgttatggt tataggcggt ggcgcagaat taatatgcga tgcagtaaaa 5640
122 aaacacacac agattcgtga tgaacgtttt ttcaaaacca ataactctca atatgattta 5700
123 gttaacggta tgtatctcat aggtaattaa tgatggacaa gcgcagaacc attgccttca 5760
124 aactaaatcc agatgtaaat caaacagata aaattgtttg tgatacactg gacagtatcc 5820
125 cgcaagggga acgaagccgc cttaaccggg ccgcactgac ggcaggtctg gccttataca 5880
126 gacaagatcc ccggacccct ttccttttat gtgagctgct gacgaaagaa accacatttt 5940
127 cagatatcgt gaatatattg agatcgctat ttccaaaaga gatggccgat tttaattctt 6000
128 caatagtcac tcaatcctct tcacaacaag agcaaaaaag tgatgaagag accaaaaaaa 6060
129 atgcgatgaa gctaataaat taattcaatt attattgagt tccctttatc cactatcagg 6120
130 ctggataaag ggaactcaat caagttattt tcttaccagt cattacataa tcgttattat 6180
131 gaaataatcg tttgcactgt ctctgttatt caggcaattt caataaaggc acttgctcac 6240
132 gctctgtcat tttctgaaac tcttcatgct g                                 6271
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 305
136 <212> TYPE: PRT
137 <213> ORGANISM: Salmonella Typhi
139 <400> SEQUENCE: 2
140 Met Thr Ser Ile Phe Ala Glu Gln Thr Val Glu Val Val Lys Ser Ala
141 1               5                   10                  15
142 Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
143             20                  25                  30
144 Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
145             35                  40                  45
146 Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
147         50                  55                  60
148 Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
149 65                  70                  75                  80
150 Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
151             85                  90                  95
152 Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
153             100                 105                 110
154 Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
155             115                 120                 125
156 Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala
```

RAW SEQUENCE LISTING   DATE: 12/03/2001
PATENT APPLICATION: US/09/993,292   TIME: 12:19:47

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\11212001\I993292.raw

```
157       130                    135                    140
158 Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
159 145                 150                    155                    160
160 Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
161                 165                    170                    175
162 Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
163                 180                    185                    190
164 Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
165             195                    200                    205
166 Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
167       210                    215                    220
168 Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
169 225                 230                    235                    240
170 Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
171                 245                    250                    255
172 Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
173             260                    265                    270
174 Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
175             275                    280                    285
176 Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
177       290                    295                    300
178 Ser
179 305
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 102
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Cloning primer
190 <400> SEQUENCE: 3
191 ggatccaaaa taaggaggaa aaaaaatga ctagtatttt tgcagaacaa actgtagagg 60
192 tagttaaaag cgcgatcgaa accgcagatg gggcattaga tc                  102
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 101
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Cloning primer
202 <400> SEQUENCE: 4
203 cctaggttat cagctagcga cgtcaggaac ctcgaaaagc gtcttcttac catgacgttg 60
204 ttggtattca ttacaggtgt taatcatttt ctttgcagct c                  101
206 <210> SEQ ID NO: 5
207 <211> LENGTH: 97
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Cloning primer
214 <400> SEQUENCE: 5
215 cacggtaaga agacgctttt cgaggttcct gacgtcgcta gctgataacc taggtcatgt 60
```

```
216 tagacagctt atcatcgata agctttaatg cggtagt                        97
218 <210> SEQ ID NO: 6
219 <211> LENGTH: 69
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Cloning primer
226 <400> SEQUENCE: 6
227 agatctacta gtgtcgacgc tagctatcag gtcgaggtgg cccggctcca tgcaccgcga 60
228 cgcaacgcg                                                        69
230 <210> SEQ ID NO: 7
231 <211> LENGTH: 60
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Cloning primer
238 <400> SEQUENCE: 7
239 actagtcacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt gggtgcacga 60
242 <210> SEQ ID NO: 8
243 <211> LENGTH: 101
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Cloning primer
250 <400> SEQUENCE: 8
251 cattaaaggt tatcgatgat aagctgtcaa acatgagcta gcctaggtca ttaccaatgc 60
252 ttaatcagtg aggcacctat ctcagcgatc tgtctatttc g                   101
254 <210> SEQ ID NO: 9
255 <211> LENGTH: 101
256 <212> TYPE: DNA
```

C--> 257 <213> ORGANISM: (Artifical sequence)
W--> 259 <220> FEATURE:
W--> 259 <223> OTHER INFORMATION:

Explanation missing — see error summary sheet, item

```
259 <400> SEQUENCE: 9
260 cgaaatagac agatcgctga gataggtgcc tcactgatta agcattggta atgacctagg 60
261 ctagctcatg tttgacagct tatcatcgat aacctttaat g                   101
263 <210> SEQ ID NO: 10
264 <211> LENGTH: 71
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Cloning primer
271 <400> SEQUENCE: 10
272 gcgcactagt aaagaaacga accaaaagcc atataaggaa acatacggca tttcccatat 60
273 tacacgccat g                                                     71
275 <210> SEQ ID NO: 11
276 <211> LENGTH: 103
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/993,292**

DATE: 12/03/2001
TIME: 12:19:48

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\11212001\I993292.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:257 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:259 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:259 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:525 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:19, CDS LOCATION: (0)...
(2253)

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09|993,292

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
     ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
     each n or Xaa can only represent a single residue. Please present the maximum number of each
     residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
     Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
     <400> sequence id number
     000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
     is Artificial Sequence

11 ✓ Use of <220>   Sequence(s) __9__ missing the <220> "Feature" and associated numeric identifiers and responses.
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
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